



SEQUENCE LISTING

<110> Bond, Christopher J.

<120> SYNTHETIC ANTIBODY PHAGE LIBRARIES

<130> 11669.136USU1

<140> 10/759,731

<141> 2004-01-16

<150> US 60/441,059

<151> 2003-01-16

<150> US 60/488,610

<151> 2003-07-18

<150> US 60/510,314

<151> 2003-10-08

<160> 194

<170> PatentIn version 3.3

<210> 1

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> 4D5 light chain variable domain

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Phe Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

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<220>
 <223> 4D5 heavy chain variable domain

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 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Val Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

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 <211> 35
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<220>
 <223> GNC4 leucine zipper

<400> 3

Gly Arg Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys
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Asn Tyr His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly
 20 25 30

Glu Arg Gly
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Tyr Ala Met Asp Tyr
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<210> 5
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<210> 6
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Ser Arg Asn Leu Ser Glu Asn Ser Tyr Ala Met
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<400> 7

Ser Arg Ala Gly Trp Ala Gly Trp Tyr Ala Met
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<220>
<223> heavy chain CDR3

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<220>
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<223> Xaa is either A, C, D, E, G, K, N, R, S, T, Y, or W

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<222> (9)..(9)
<223> Xaa is any naturally occurring amino acid

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<223> Xaa is any naturally occurring amino acid

<400> 12

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<220>
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<222> (28)..(28)
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<223> m is a or c

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<222> (30)..(30)
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<222> (31)..(31)
<223> k is g or t

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<221> misc_feature

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<222> (28)..(28)

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<223> k is g or t

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<211> 72

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<223> m is a or c

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 <222> (34)..(34)
 <223> d is a, g, or t

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 agcgtcaagg gc 72

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 <223> m is a or c

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<210> 18
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 <223> single chain Fv

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 aggaccatag attatgaaaa taaaaacagg tgcacgcattc ctcgcattat ccgcattaac 180

| | |
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| gacgatgatg ttttccgcct cggcttatgc atccgatatc cagatgaccc agtccccgag | 240 |
| ctccctgtcc gcctctgtgg gcgatagggg caccatcacc tgccgtgcca gtcaggatgt | 300 |
| gaatactgct gtagcctggg atcaacagaa accaggaaaa gctccgaagc ttctgattta | 360 |
| ctcggcatcc ttctctact ctggagtccc ttctcgcttc tctggtagcc gttccgggac | 420 |
| ggattttcact ctgaccatca gcagtctgca gccggaagac ttcgcaactt attactgtca | 480 |
| gcaacattat actactcctc ccacgttcgg acagggtacc aagggtggaga tcaaacgga | 540 |
| tatgccgatg gctgatccga accgtttccg cggtaagaac ctggtttttc attctgagat | 600 |
| ctccgagggt cagctgggtg agtctggcgg tggcctgggtg cagccagggg gtcactccg | 660 |
| tttgtcctgt gcagcttctg gcttcaacat taaagacacc tatatacact ggggtgcgtca | 720 |
| ggccccgggt aagggcctgg aatgggttgc aaggatttat cctacgaatg gttatactag | 780 |
| atatgccgat agcgtcaagg gccgtttcac tataagcgca gacacatcca aaaacacagc | 840 |
| ctacctaaa atgaacagct taagagctga ggacactgcc gtctattatt gtagccgctg | 900 |
| gggaggggac ggcttctatg ctatggacta ctgggggtcaa ggaacactag tcaccgtctc | 960 |
| cagcagtggc ggtggctctg gttccggtga ttttgattat gaaaagatgg caaacgctaa | 1020 |
| taagggggct atgaccgaaa atgccgatga aaacgcgcta cagtctgacg ctaaaggcaa | 1080 |
| acttgattct gtcgctactg attacggtgc tgctatcgat ggtttcattg gtgacgtttc | 1140 |
| cggccttgct aatggtaatg gtgctactgg tgattttgct ggctctaatt cccaaatggc | 1200 |
| tcaagtcggt gacggtgata attcaccttt aatgaataat ttccgtcaat atttaccttc | 1260 |
| cctccctcaa tcggttgaat gtcgcccttt tgtctttagc gctggtaaac catatgaatt | 1320 |
| ttctattgat tgtgacaaaa taaacttatt ccgtgggtgtc tttgcgtttc ttttatatgt | 1380 |
| tgccaccttt atgtatgtat tttctacgtt tgctaacata ctgcgtaata aggagtctta | 1440 |
| a | 1441 |

<210> 19

<211> 1588

<212> DNA

<213> Artificial Sequence

<220>

<223> single chain Fv with zipper domain

<400> 19

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| aggaccatag attatgaaaa taaaaacagg tgcacgcata ctcgcattat ccgcattaac | 180 |

| | |
|--|------|
| gacgatgatg ttttccgcct cggcttatgc atccgatatc cagatgaccc agtccccgag | 240 |
| ctccctgtcc gcctctgtgg gcgatagggc caccatcacc tgccgtgcca gtcaggatgt | 300 |
| gaatactgct gtagcctggt atcaacagaa accaggaaaa gctccgaagc ttctgattta | 360 |
| ctcggcatcc ttcctctact ctggagtcct ttctcgcttc tctggtagcc gttccgggac | 420 |
| ggatttcact ctgaccatca gcagtctgca gccggaagac ttcgcaactt attactgtca | 480 |
| gcaacattat actactcttc ccacgttcgg acagggtacc aagggtggaga tcaaactcgg | 540 |
| tatgccgatg gctgatccga accgtttccg cggtaagaac ctgggtttttc attctgagat | 600 |
| ctccgagggt cagctgggtg agtctggcgg tggcctgggt cagccagggg gtcactccg | 660 |
| tttgtcctgt gcagcttctg gcttcaacat taaagacacc tatatacact ggggtgcgtca | 720 |
| ggccccgggt aagggcctgg aatgggttgc aaggatttat cctacgaatg gttatactag | 780 |
| atatgccgat agcgtcaagg gccgtttcac tataagcgca gacacatcca aaaacacagc | 840 |
| ctacctaaa atgaacagct taagagctga ggacactgcc gtctattatt gtagccgctg | 900 |
| gggaggggac ggcttctatg ctatggacta ctggggctca ggaacactag tcaccgtctc | 960 |
| cagcacatgc ccgccgtgcc cagcaccaga actgctgggc ggccgcatga aacagctaga | 1020 |
| ggacaaggtc gaagagctac tctccaagaa ctaccaccta gagaatgaag tggcaagact | 1080 |
| caaaaaactt gtcggggagc gcggaaagct tagtggcggg ggctctgggt ccggtgattt | 1140 |
| tgattatgaa aagatggcaa acgctaataa gggggctatg accgaaaatg ccgatgaaaa | 1200 |
| cgcgctacag tctgacgcta aaggcaaact tgattctgtc gctactgatt acggtgctgc | 1260 |
| tatcgatggc ttcatgtgtg acgtttccgg ccttgctaag ggtaatgggt ctactgggtg | 1320 |
| ttttgctggc tctaattccc aaatggctca agtcggtgac ggtgataatt cacctttaat | 1380 |
| gaataatttc cgtcaatatt taccttccct cctcaatcg gttgaatgtc gcccttttgt | 1440 |
| ctttagcgct ggtaaaccat atgaattttc tattgattgt gacaaaataa acttattccg | 1500 |
| tgggtgtctt gcgtttcttt tatatgttgc cacctttatg tatgtatttt ctacgtttgc | 1560 |
| taacatactg cgtaataagg agtcttaa | 1588 |

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<211> 2239

<212> DNA

<213> Artificial Sequence

<220>

<223> Fab fragment

<400> 20

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|---|------|
| acaatttcac acaggaaaca gccagtccgt ttaggtgttt tcacgagcac ttcaccaaca | 120 |
| aggaccatag attatgaaaa taaaaacagg tgcacgcatc ctcgcattat ccgcattaac | 180 |
| gacgatgatg ttttccgcct cggcttatgc atccgatatc cagatgaccc agtccccgag | 240 |
| ctccctgtcc gcctctgtgg gcgatagggt caccatcacc tgccgtgcca gtcaggatgt | 300 |
| gaatactgct gtagcctggg atcaacagaa accaggaaaa gctccgaagc ttctgattta | 360 |
| ctcggcatcc ttctctact ctggagtccc ttctcgcttc tctggtagcc gttccgggac | 420 |
| ggatttcact ctgaccatca gcagtctgca gccggaagac ttcgcaactt attactgtca | 480 |
| gcaacattat actactctc ccacgttcgg acagggtacc aaggtggaga tcaaacgaac | 540 |
| tgtggctgca ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac | 600 |
| tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa | 660 |
| ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa | 720 |
| ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca | 780 |
| caaagtctac gcctgcgaag tcacccatca gggcctgagc tcgcccgtca caaagagctt | 840 |
| caacagggga gagtgtggtg ccagctccgg tatggctgat ccgaaccgtt tccgcggtaa | 900 |
| ggacctggca taactcgagg ctgacacctc acgccggacg catcgtggcc ctagtacgca | 960 |
| agttcacgta aaaagggtaa ctagagggtg aggtgatttt atgaaaaaga atatcgcat | 1020 |
| tcttcttgca tctatgttcg ttttttctat tgctacaaac gcgtacgtg agatctccga | 1080 |
| ggttcagctg gtggagtctg gcggtggcct ggtgcagcca gggggctcac tccgtttgtc | 1140 |
| ctgtgcagct tctggcttca acattaaaga cacctatata cactgggtgc gtcaggcccc | 1200 |
| gggtaagggc ctggaatggg ttgcaaggat ttatcctacg aatgggtata ctagatatgc | 1260 |
| cgatagcgtc aagggccgtt tcactataag cgcagacaca tccaaaaaca cagcctacct | 1320 |
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| ctccaccaag ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg | 1500 |
| cacagcggcc ctgggctgcc tgggtcaagga ctacttcccc gaaccgggtga cgggtgcgtg | 1560 |
| gaactcaggc gccctgacca gcggcgtgca caccttcccc gctgtcctac agtcctcagg | 1620 |
| actctactcc ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta | 1680 |
| catctgcaac gtgaatcaca agcccagcaa caccaaggtc gacaagaaag ttgagcccaa | 1740 |
| atcttgtgac aaaactcacc tcagtggcgg tggctctggg tccggtgatt ttgattatga | 1800 |
| aaagatggca aacgctaata agggggctat gaccgaaaat gccgatgaaa acgcgctaca | 1860 |

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| gtctgacgct aaaggcaaac ttgattctgt cgctactgat tacggtgctg ctatcgatgg | 1920 |
| tttcattggg gacgtttccg gccttgctaa tggtaatggg gctactggg atttttgctgg | 1980 |
| ctctaattcc caaatggctc aagtcgggtga cggtgataat tcacctttaa tgaataat | 2040 |
| ccgtcaatat ttaccttccc tccctcaatc ggttgaatgt cgcccttttg tcttttagcgc | 2100 |
| tggtaaacca tatgaat | 2160 |
| tttt ctattgattg tgacaaaata aacttattcc gtggtgtctt | 2160 |
| tgcgtttctt ttatatgttg ccacctttat gtatgtat | 2220 |
| ttt tctacgtttg ctaacatact | 2220 |
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<210> 21
 <211> 2383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fab fragment with zipper domain

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| aggaccatag attatgaaaa taaaaacagg tgcacgcac ctcgcattat ccgcattaac | 180 |
| gacgatgatg ttttccgcct cggcttatgc atccgatatc cagatgaccc agtccccgag | 240 |
| ctccctgtcc gcctctgtgg gcgatagggt caccatcacc tgccgtgcca gtcaggatgt | 300 |
| gaatactgct gtagcctggg atcaacagaa accaggaaaa gctccgaagc ttctgattta | 360 |
| ctcggcatcc ttctctact ctggagtccc ttctcgcttc tctggtagcc gttccgggac | 420 |
| ggatttcact ctgaccatca gcagtctgca gccggaagac ttcgcaactt attactgtca | 480 |
| gcaacattat actactcctc ccacgttcgg acagggtacc aagggtggaga tcaaacgaac | 540 |
| tgtggctgca ccatctgtct tcatcttccc gccatctgat gagcagttga aatctggaac | 600 |
| tgctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag tacagtggaa | 660 |
| ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc aggacagcaa | 720 |
| ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact acgagaaaca | 780 |
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| caacagggga gagtgtggtg ccagctccgg tatggctgat ccgaaccgtt tccgcggtaa | 900 |
| ggacctggca taactcgagg ctgatcctct acgccggacg catcgtggcc ctagtacgca | 960 |
| agttcacgta aaaagggtaa ctagagggtg aggtgatttt atgaaaaaga atatcgcat | 1020 |
| tcttcttgca tctatgttcg ttttttctat tgctacaaac gcgtacgctg agatctccga | 1080 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Phe | Asp | Tyr |
| 1 | | | | 5 | | | | | | 10 |

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| Ala | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Tyr | Xaa | Met | Asp | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

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| 1 | | | | 5 | | | | | | 10 | | | | 15 | |

Tyr

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1 5 10

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Thr Thr Ser Asn Gly
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Ala Tyr Ser Ser Asn Tyr Tyr Arg
1 5

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Ala Arg Trp Ser Arg Ala Ser Phe Tyr
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Thr Thr Gly Thr Asp
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Thr Thr Asp Ser Gly
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Gly Arg Ser Tyr Ser Ser Asn Arg
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Ala Lys Trp Pro Trp Tyr Asn Ala Trp
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Gly Tyr Ser Tyr Gly Thr Arg
1 5

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Thr Thr Gly Asn Ala
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Thr Asn Asp Tyr Tyr
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Thr Ser Asn Thr Gly
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Thr Thr Ser Tyr Gly
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Ala Ser Ser Tyr Ser Tyr Arg
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Gly Tyr Asn Ser Gly Ser Arg
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<400> 92

Thr Ser Ser Ser Ala
1 5

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Ala Trp Ser Asn Gly Ser Arg
1 5

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Ala Xaa Thr Ala Gly Gly Ala Lys Tyr
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<400> 95

Thr Thr Asn Thr Trp
1 5

<210> 96
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<400> 96

Gly Asp Tyr Asp Gly Tyr Arg
1 5

<210> 97
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Ala Xaa Trp Arg Trp Trp Gly Arg Tyr
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<400> 98

Thr Asn Gly Asn Tyr
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Gly Trp Ser Asn Gly Tyr Arg
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Gly Arg Ser Tyr Asn Tyr Arg
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Thr Thr Ser Asn Asp
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Ala Trp Ser Tyr Asn Tyr Arg
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Val Ala Thr Tyr Tyr Asn
1 5

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Trp Gly Ala Lys Gly Thr Trp
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Asn Ala Asp Ser Ala
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Tyr Ala Tyr Asp Tyr Tyr
1 5

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Asn Asp Asn Thr Ala
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Val Ser His Asp Thr Tyr
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Ala Ala Ala Trp Ala Ser Tyr
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Val Tyr His Asp Lys Tyr
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Trp Trp Tyr Ser Trp Asn Trp
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cgggtaaaga acgtgaatcg gttgccgcca ttaactggga ttcggctcgt acttactatg 180
cttcgtccgt ccggtggtcgt tttactatctt cacgtgataa tgccaaaaaa actgtctatt 240
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr
20 25 30

Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val
35 40 45

Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr
52

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65 | | 70 | | 75 | | 80 | | | | | | | | | |
| Leu | Gln | Met | Asn | Ser | Leu | Lys | Pro | Glu | Asp | Thr | Ala | Val | Tyr | Thr | Cys |
| | | | 85 | | | | | | 90 | | | | 95 | | |
| Gly | Ala | Gly | Glu | Gly | Gly | Thr | Trp | Asp | Ser | Trp | Gly | Gln | Gly | Thr | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Thr | Val | Ser | Ser | Ala | Gly | Gly | Met | Asp | Tyr | Lys | Asp | Asp | Asp | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |

Lys

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| Cys | Gly | Ala | Gly | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
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Arg Ile Xaa Cys

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<220>
<223> VHH RIG C terminal sequence

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Cys Trp Val Thr Trp
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<223> Xaa is I, L, V, R, W, or S

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<223> Xaa is any naturally occurring amino acid, wherein there can be 1
or more deletions up to 16 deletions

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<222> (20)..(20)
<223> Xaa is W, G, R, M, S, or A

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<222> (21)..(21)
<223> Xaa is V, L, P, G, S, E or W

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1 5 10 15

Xaa Xaa Xaa Xaa Xaa
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 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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      or more deletions up to 16 deletions

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<223> Xaa is any naturally occurring amino acid

<400> 142

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10     15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20     25

<210> 143
<211> 24
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<220>
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 deletion up to 19 deletions

<400> 143

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Xaa | Arg | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| 1 | | | 5 | | | | 10 | | | | | 15 | | |

| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
| | | | | | | | 20 |

<210> 144
 <211> 23
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 or more deletions up to 14 deletions

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 <223> Xaa is any naturally occurring amino acid

<220>
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<223> Xaa is V, L, or P

<220>

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<223> Xaa is any naturally occurring amino acid

<400> 144

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Trp Xaa Xaa Xaa Xaa Xaa
20

<210> 145

<211> 17

<212> PRT

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<400> 145

Arg Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Val Xaa
1 5 10 15

Xaa

<210> 146

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<400> 146

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Phe | Xaa | Arg | Val | Xaa |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |

Xaa

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<400> 147

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| 1 | | | 5 | | | | | 10 | | | | | | 15 | |

Xaa

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<400> 148

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Trp | Xaa | Xaa | Leu | Xaa |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |

Xaa

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<400> 149

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| Arg | Ile | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Cys | Trp | Val | Xaa | Xaa |
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 <220>
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 <400> 150

Arg Xaa Xaa Arg
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<210> 151
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 <223> s is g or c

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 <223> r is a or g

<220>
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 <223> k is g or t

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 <223> s is g or c

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<223> m is a or c

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<222> (43)..(43)

<223> k is g or t

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<212> DNA

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<222> (37)..(38)

<223> n is a, g, c, or t

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<222> (39)..(39)

<223> s is g or c

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<222> (43)..(44)

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<222> (45)..(45)

<223> s is g or c

<400> 152

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<210> 153

<211> 60

<212> DNA

<213> Artificial Sequence

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<222> (18)..(18)

<223> s is g or c

<400> 153

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<210> 154

<211> 87

<212> DNA

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<223> s is g or c

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nnsnnsnnsn nsnnstgggg tcagggt                                           87

<210> 155
<211> 87
<212> DNA
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<220>
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<220>
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<223> r is a or g

<220>
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<222> (29)..(29)
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<220>
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<222> (32)..(32)
<223> s is g or c

<220>
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<222> (34)..(35)
<223> s is g or c

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<222> (37)..(37)
<223> k is g or t

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 <222> (74)..(74)
 <223> s is g or c

<400> 155
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kccksggytr ctksgtgggg tcagggt 87

<210> 156
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 <222> (29)..(29)
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 <222> (31)..(31)
 <223> r is a or g

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<222> (32)..(32)
<223> m is a or c

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<223> s is g or c

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 <223> m is a or c

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 rctsstgyts makcctgggg tcagggt 87

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 <213> Artificial Sequence

<220>
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 <223> y is c or t

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kytgstsytg ytgsttgggg tcagggt 87

<210> 158
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<220>
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 <223> k is g or t

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 <222> (59)..(59)
 <223> s is g or c

<220>
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 <222> (62)..(62)
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 <222> (64)..(64)
 <223> r is a or g

<220>
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 <222> (65)..(65)
 <223> y is c or t

<220>
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 <222> (67)..(67)
 <223> s is g or c

<220>
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 <222> (70)..(70)
 <223> s is g or c

<220>
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 <222> (71)..(71)
 <223> y is c or t

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 gmarygscas ytgcgtaggg tcaggg 86

<210> 159
 <211> 4
 <212> PRT

<213> Artificial Sequence

<220>

<223> N terminal sequence of CDRH3 scaffold

<220>

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<400> 159

Arg Ile Xaa Cys

1

<210> 160

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> C terminal sequence of CDRH3 scaffold

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<223> Xaa is any naturally occurring amino acid

<400> 160

Phe Xaa Arg Val

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<210> 161

<211> 4

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<213> Artificial Sequence

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Trp Xaa Xaa Leu

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<210> 162

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<223> C terminal sequence of CDRH3 scaffold

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Trp Xaa Met Pro

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<210> 163

<211> 17

<212> PRT

<213> Artificial Sequence

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<400> 163

Arg Ile Gly Arg Ser Val Phe Asn Leu Arg Arg Glu Ser Trp Val Thr

1

5

10

15

Trp

<210> 164

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> CDRH3

<400> 164

Leu Leu Arg Arg Gly Val Asn Ala Thr Pro Asn Trp Phe Gly Leu Val

1

5

10

15

Gly

<210> 165

<211> 17

<212> PRT

<213> Artificial Sequence

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<223> CDRH3

<400> 165

Val Leu Lys Arg Arg Gly Ser Ser Val Ala Ile Phe Thr Arg Val Gln
1 5 10 15

Ser

<210> 166

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3

<400> 166

Arg Leu Val Asn Gly Leu Ser Gly Leu Val Ser Trp Glu Met Pro Leu
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Ala

<210> 167

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3

<400> 167

Phe Val Ala Gly Pro Trp Trp Trp Arg Trp Arg Thr Pro Ser Gly Val
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Ala

<210> 168

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDRH3

<400> 168

Val Leu Glu Leu Arg Ser Ser Gly Gly Asn Ala Arg Trp Met Ser Leu
1 5 10 15

Tyr

<210> 169
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 169

Leu Arg Ile Ser Pro Tyr Ala Phe Trp Leu Gly Thr Trp Ala Pro Ser
1 5 10 15

Tyr

<210> 170
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRH3

<400> 170

Leu Trp Thr Arg Ala Arg Ser Trp Arg Trp Trp Trp Arg Arg Glu Gln
1 5 10 15

Phe

<210> 171
<211> 17
<212> PRT
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<220>
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<400> 171

Trp Arg Ser Trp Ile Ser Ser Ile Leu Gly Leu Arg Thr Trp Trp Tyr
1 5 10 15

Ala

<210> 172

<211> 17
<212> PRT
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<220>
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<400> 172

Lys Ser Thr Arg Trp Arg Ala Gly His Gly Arg Thr Phe His Trp Leu
1 5 10 15

Ser

<210> 173
<211> 14
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<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

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<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

<400> 173

Ala Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Tyr Ala Met Asp Tyr
1 5 10

<210> 174
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<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

<400> 174

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1 5 10

<210> 175

<211> 14

<212> PRT

<213> Artificial Sequence

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<223> F141

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<222> (9)..(9)

<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

<400> 175

Ala Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Tyr Ala Met Asp Tyr
1 5 10

<210> 176

<211> 14

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<223> F142

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<222> (3)..(8)

<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

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<210> 177

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> F170

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<223> Xaa is A, C, D, G, H, N, P, R, S, T, or Y

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1 5

<210> 178

<211> 12

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1 5 10

<210> 179

<211> 13

<212> PRT

<213> Artificial Sequence

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<223> F171b

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<210> 180

<211> 14

<212> PRT

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<223> F181

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<211> 14

<212> PRT

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<223> F179

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<211> 15

<212> PRT

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<223> F182

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<210> 183
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<223> F185

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Ala Xaa Xaa Xaa Xaa Xaa Phe Xaa Tyr

1 5

<210> 186

<211> 15

<212> PRT

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<222> (12)..(12)

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<400> 186

Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Met Asp Tyr

1 5 10 15

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 <223> Xaa is W, S, A, or G

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 <222> (13)..(13)
 <223> Xaa is A, V, or G

<400> 187

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Met | Asp | Tyr |
| 1 | | | | 5 | | | | | | 10 | | | | 15 | |

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<400> 188

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1 5 10 15

Tyr

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Trp Gly Gly Asp Gly Phe Tyr
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Ser Arg Trp Gly Xaa Xaa Xaa Xaa Xaa Ala Met Asp Tyr
1 5 10

<210> 191
<211> 5
<212> PRT
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Asn Ala Asp Ser Ala
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<223> mVEGF 174

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Thr Gly Gly Ser Trp
1 5

<210> 193
<211> 25
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<223> Xaa is I, L, or V

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<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is any naturally occurring amino acid

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<222> (4)..(4)
<223> Xaa is C, R, or N

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<221> MISC_FEATURE
<222> (5)..(20)
<223> Xaa is any naturally occurring amino acid, wherein there can be 1
or more deletions up to 15 deletions

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<222> (21)..(21)
<223> Xaa is C, S, F, T, E, or D

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<222> (22)..(22)
<223> Xaa is W, G, R, or M

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<222> (24)..(24)
<223> Xaa is T, V, L, or Q

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<222> (25)..(25)
<223> Xaa is W, G, or S

<400> 193

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25

<210> 194
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<400> 194

Arg Ile Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Trp Val Xaa Xaa

1

5

10

15